



7

1

SEQUENCE LISTING

<110> FARWICK, MIKE
HUTHMACHER, KLAUS
PFEFFERLE, WALTER

<120> NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE MIKE17 GENE

<130> 21123/280108/MAS

<140> 09/825,293

<141> 2001-04-04

<150> DE 100 47 867.0

<151> 2000-09-27

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1890

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (252)..(1673)

<223> mike17-Gen

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ctttgcgag gtgacacaat tatcccaaca gttgcaccgt aggtgcctaa aaagttcccg 120
gggcggatgt ggcccgacca cgccgggcac ctggtggcgg cgggctgcgt cgaaaagcga 180
aatcaacaa gtttgcaaca cctcagtgcc aagagtgggt aaggtgatgg tgatcacgct 240
atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290
Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu
1 5 10
cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338
Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly
15 20 25
tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386
Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu
30 35 40 45
acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434
Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala
50 55 60
acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482
Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln
65 70 75

AI
Cm T

gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530
 Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln
 80 85 90

gag ctt tcg gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg 578
 Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met
 95 100 105

gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc 626
 Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile
 110 115 120 125

gca gtg gat aat cgc acc aac acg cct gag gaa cgc cgt ccc atc gcg 674
 Ala Val Asp Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala
 130 135 140

gag gcc gtg agc atg ccg cac gaa gag gtc cgc gat ttc att tac gcc 722
 Glu Ala Val Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala
 145 150 155

cgc caa aac tac ttc gat gcc ctt gac cgc cgc gcc gaa gcc atc gcc 770
 Arg Gln Asn Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala
 160 165 170

gcg caa ctg ggc tgg cag ccg tac gat tcc cgc gcc atg gaa gat tcg 818
 Ala Gln Leu Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser
 175 180 185

atc gcc cgc cgc ctg caa atg gat cac gat gtc acc atc acc tcc tcc 866
 Ile Ala Arg Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser
 190 195 200 205

aaa gag gaa tcc ggc acg ctg cac cac ttc gac ccc gag acg cgt ctg 914
 Lys Glu Glu Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu
 210 215 220

ctg aca atc cac gca cgc ctc aac ccc ggg caa cgc gcc ttc cgc atg 962
 Leu Thr Ile His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met
 225 230 235

gcc acc gaa ctc ggc tac cta gaa gcc aac gac ctc atc gaa ggt atc 1010
 Ala Thr Glu Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile
 240 245 250

gtt gac gac ggc atc tgg tcc acc ccc gaa gcc cgc acc cta gcc atc 1058
 Val Asp Asp Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile
 255 260 265

cgc ggt gtg gcc tcc tac ttc gcc gcc gcc gtg atg ctg ccc tac aaa 1106
 Arg Gly Val Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys
 270 275 280 285

atc ttc cac tcc gag gcc gaa aaa tcc ggc tac gac atc gag tac cta 1154
 Ile Phe His Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu
 290 295 300

A1
 Cm. x

ggc caa ctc ttt ggc gtg ggc tat gag aca acc gcc cac cgc ttg tcc 1202
 Gly Gln Leu Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser
 305 310 315
 acc ctg cag cgc ccc aac ctg cgc ggc atc ccc ttt acc ttc gtg cgc 1250
 Thr Leu Gln Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg
 320 325 330
 gtc gac cgc gcc ggc aac atg tcc aaa cgc caa tcc gcc acc ggc ttc 1298
 Val Asp Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe
 335 340 345
 cac ttc acc cac tac ggc ggc acc tgc ccc ctg tgg aac gtg ttt gaa 1346
 His Phe Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu
 350 355 360 365
 acc ttc acc aac ccc ggc caa gtg ctc cgc caa ttc gcg caa atg ccc 1394
 Thr Phe Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro
 370 375 380
 gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa 1442
 Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu
 385 390 395
 gcc cgg ttc ggc gaa gta gac aaa atg ttc gcc atc ggc ctg ggc tgc 1490
 Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys
 400 405 410
 gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc 1538
 Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu
 415 420 425
 cag gac ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc 1586
 Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys
 430 435 440 445
 acc cgc gag aac tgc gcg cag cgc gca ttc cca tcc gtc cac ggc cgc 1634
 Thr Arg Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg
 450 455 460
 atc aac atc gac gcg cac gaa tcc act atc gcg ccg tac taagaaaagg 1683
 Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
 465 470
 agcttgcttt acgacgcacc ctgcgggggt ggggttttacc ttttatgaat gatcagcaat 1743
 atccgcgtaa acaccatcgg tagccagaag aacatcatcc ggggcgataa tcagggacca 1803
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<211> 474

<212> PRT

<213> Corynebacterium glutamicum

AI
Cm.1

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 Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro
 35 40 45
 Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe
 50 55 60
 Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met
 65 70 75 80
 Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser
 85 90 95
 Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met
 100 105 110
 His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp
 115 120 125
 Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val
 130 135 140
 Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn
 145 150 155 160
 Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu
 165 170 175
 Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser Ile Ala Arg
 180 185 190
 Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu
 195 200 205
 Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile
 210 215 220
 His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu
 225 230 235 240
 Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile Val Asp Asp
 245 250 255
 Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val
 260 265 270
 Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His
 275 280 285
 Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu
 290 295 300

AI
 Crit

Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln
305 310 315 320

Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg
325 330 335

Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr
340 345 350

His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr
355 360 365

Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg
370 375 380

Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe
385 390 395 400

Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg
405 410 415

His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu
420 425 430

Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu
435 440 445

Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn Ile
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Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
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<212> DNA

<213> Corynebacterium glutamicum

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<223> Primer mikE17-int1

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<213> Corynebacterium glutamicum

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<223> Primer mikE17-int2

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AI
Cancelled